by the different dependences of these two time scales on the load. The model further reveals the dependence of the motor dynamics on the number of stators. In particular, we show that the maximum speed of the motor is independent of the number of stators, which agrees with recent resurrection experiments at near zero loads (Yuan & Berg, PNAS 105, 1182-1185, 2008). We have also used the model to study stepping statistics in single flagellar motor and different noise sources for rotational speed fluctuation. In general, we believe the model maybe useful to study other molecular motor systems with multiple asynchronous power generating units. [Part of the work was published in (Meacci & Tu, PNAS 106, 3746-3751, 2009)].

824-Pos

Understanding Kink Propagation in Spiroplasma

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Spiroplasma are helical bacteria of the class Mollicutes, that lack cell walls and swim by propagating a kink of handedness-change along their helical shaped body. Recent microscopy studies indicate that the major structural component of the cell is a multistranded protein ribbon, bound to the inner cell membrane. The ribbon runs along the whole cell body, following the shortest helical path on the membrane inner surface. Kink propagation is believed to be driven by conformational changes in the ribbon subunits (itself possibly driven by unidentified motor proteins), but the microscopic mechanism is largely unknown. We use simple mechanical models to understand kink propagation in Spiroplasma. Our conclusions differ from earlier work based on purely geometrical considerations in several important ways. This leads us to propose new microscopic mechanisms for the handedness change, and a new interpretation of the observed bend angle in kinked cells.

We further model the mechanochemistry of kink propagation, and find that the kink speed might be limited either by protein friction or a chemical event in the mechanochemical cycle of a ribbon subunit. The two mechanisms might be distinguished based on the randomness of the kink propagation.

Our results offer a qualitatively new understanding of existing observations, and several useful suggestions for future experiments.

825-Pos

Swimming Hydrodynamics of a Run-And-Tumble Bacterium with Helical Flagella

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To study the swimming of a peritrichous bacterium such as Escherichia coli, which is able to change its swimming direction actively, we simulate the ''run-and-tumble'' motion using a bead-spring model to account for the hydrodynamic and the mechanical interactions between the cell body and multiple flagella, the reversal of the rotation of a flagellum in a tumble and the associated polymorphic transformations of the flagellum. The cell body and each flagellum are connected by a flexible hook, so that the flagella can take independent orientations with respect to the cell body. This simulation reproduces the experimentally observed behaviors of E. coli, namely, a three-dimensional random-walk trajectory in run-and-tumble motion and steady clockwise swimming near a wall. We show that the polymorphic transformation of a flagellum in a tumble facilitates the reorientation of the cell, and that the time-averaged flow field near a cell in a run has double-layered helical streamlines, with a time-dependent flow magnitude large enough to affect the transport of surrounding chemoattractants. This new model, which can be refined by using more beads if more quantitative predictions are desired, strikes a balance between accuracy and simplicity that will permit it to be used to determine the migration behavior of particles near a swimming cell, cell-cell hydrodynamic interactions, the effect of the number and geometric distribution of flagella on migration, the mechanism of circular swimming near a wall, details of the tumbling motion, and the effect of the Brownian motion on swimming. We also develop minimal models, inspired by the simple model of Najafi and Golestanian, that contain only 3-5 beads, and can simulate simple ''pusher'' and ''puller'' micro-swimmers, and are also able to include helical flow typically produced by rotary flagellar motion.

826-Pos

Swimming Microorganisms in Gels

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Many swimming microorganisms must move through viscoelastic fluids and gels. I present work on swimming in gels. First, unlike incompressible fluids, a gel can have compressional modes with relative motion between polymer and solvent fractions. In a continuum model for a gel, we show that compressibility can increase the swimming speed of Taylor's swimming sheet. The zero-frequency shear modulus of a gel requires altered boundary conditions on the swimmer. Second, many biological gels are heterogeneous on the lengthscale of swimming microorganisms, necessitating non-continuum models that treat the gel network and swimmer on equal footing. We show that a random network modeled as dilute, immobile spherical obstacles increases the average swimming speed of a Golestanian three-sphere swimmer.

827-Pos

A Tug-of-War Mechanism for Bacterial Surface Movement

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In various bacterial species surface motility is mediated by cycles of type IV pilus motor adhesion and force generation, but it is unclear whether multiple motors cooperate mediate movement. Here we show that 7 ± 1 pili/cell are required for persistent movement of *Neisseria gonorrhoeae* with MSD $\sim t^{1.5 \pm 0.1}$. The unbinding force of individual pili from the surface $F < 30$pN was considerably lower than the stalling force $F > 100$pN, suggesting that density, force, and adhesive properties of the pilus motor have evolved to enable a tug-of-war mechanism for bacterial movement. Consistently, we found that bacteria were unable to move on fluid lipid membranes, most likely because force generation was not translated into bacterial movement due to slippage. Using microcontact printing, we confined the surface motility and microcolony formation to non-fluid islands within a fluid lipid membrane. Our patterning technique used physico-chemical surface properties that did not interfere with bacterial tug-of-war mediated motility and we anticipate that it will be useful for studying differentiation and gene expression within dynamical bacterial clusters and biofilms.

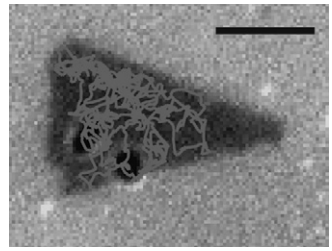

Figure: BSA-triangles on coverslides surrounded by with a DOPC membrane. The trace shows a path over 2min. Scale bar: 5μm.

828-Pos

Examples of X-Ray Scattering Studies of Biological Systems under Extreme Conditions

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Biological systems under extreme conditions often resort to unusual structures to achieve special functions for survival. The ''bioengineering'' principles of such ''extreme'' structures may inspire biomimic designs of functional materials. Here we give several examples of such naturally occurring unusual structures probed with x-ray scattering. i) In bacterial spores, the spore coat appears to comprise of laminar layers of quasi-2D crystals with periodicity of ~1 nm. Such ordered assembly may be responsible for the spore resistance to heat, toxic chemicals, and mechanical disruption. ii) In starved bacterial cells, the DNA packaging protein (DPS) is over-produced to compact the chromosomal DNA close to crystalline density to protect the genomic integrity and facilitate homologous recombination. iii) In bacterial cells with over-produced DNA, mild treatment with antibiotics can lead to liquid-crystalline DNA that responds to external osmotic stress. Future work includes 1) uncovering the molecular basis of characterized structures and 2) extending into systems such as cells under radiation or heat and cancer cells.

829-Pos

Redundant Mechanisms for Stable Cell Locomotion Revealed by Minimal Models

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Crawling of eukaryotic cells on flat surfaces is underlain by the dynamics of the actin network and graded adhesion to the substrate and is regulated via a complex biochemical network. Some crawling cells maintain roughly constant shape and velocity. The paradigm of this stable crawling is the fish keratocyte, a rapidly moving cell that maintains a half-moon shape while translocating. Here we use moving boundary simulations to explore 4 different, minimal mechanisms for cell locomotion and show that all of these are sufficient to produce steady shapes and movements with resulting features that resemble the keratocyte morphology. We begin by considering a diffusion-limited actin model where G-actin transport to the leading edge controls the rate of protrusion of the leading edge.